

Figure 1 (SEQ ID NO: 2878)

GATCAAACCTCTTTCCATTGAGAGTCCTCTGATTGAGATTTAATGTTAACATTTTGGGAAGACAGTATTCAGAAAAAAATTTCC  
TTAATAAAAAATACAACCTGAGATCCTTCAAATATGAACTGGTTGGGGAATCTCCATTTTTCAATATTATTTCTTCTTGTTTTTC  
TTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAAC  
TGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACAGCAAAGGAA  
AATAAACACAGAATATAATAAATGAGATAATCTAGCTTAAACTATAACTTCCTCTTTAGAACTCCAACCACATTGATC

FIG. 2A (SEQ ID NOS: 2879 &amp; 2880)

5' 9 18 27 36 45 54  
 CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 63 72 81 90 99 108  
 ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 117 126 135 144 153 162  
 TGG TCA CAG TTC AGC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 M M V D P N G N E S S  
 171 180 189 198 207 216  
 GCT ACA TAC TTC ATC CTA ATA GGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 A T Y F I L I G L P G L E E A Q F W  
 225 234 243 252 261 270  
 TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 L A F P L C S L Y L I A V L G N L T  
 279 288 297 306 315 324  
 ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 I I Y I V R T E H S L H E P M Y I F  
 333 342 351 360 369 378  
 CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 L C M L S G I D I L I S T S S M P K  
 387 396 405 414 423 432  
 ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 M L A I F W F N S T T I Q F D A C L  
 441 450 459 468 477 486  
 CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 L Q I F A I H S L S G M E S T V L L  
 495 504 513 522 531 540  
 GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 A M A F D R Y V A I C H P L R H A T  
 549 558 567 576 585 594  
 GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 V L T L P R V T K I G V A A V V R G  
 603 612 621 630 639 648  
 GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 A A L M A P L P V F I K Q L P F C R

FIG. 2B

|                                     |                 |                 |                 |         |      |
|-------------------------------------|-----------------|-----------------|-----------------|---------|------|
| 657                                 | 666             | 675             | 684             | 693     | 702  |
| TCC AAT ATC CTT TCC                 | CAT TCC TAC TGC | CTA CAC CAA GAT | GTC ATG AAG CTG | GCC     |      |
| S N I L S H S Y C L H Q D V M K L A |                 |                 |                 |         |      |
| 711                                 | 720             | 729             | 738             | 747     | 756  |
| TGT GAT GAT ATC CGG                 | GTC AAT GTC GTC | TAT GGC CTT ATC | GTC ATC ATC TCC | GCC     |      |
| C D D I R V N V V Y G L I V I I S A |                 |                 |                 |         |      |
| 765                                 | 774             | 783             | 792             | 801     | 810  |
| ATT GGC CTG GAC TCA                 | CTT CTC ATC TCC | TTC TCA TAT CTG | CTT ATT CTT AAG | ACT     |      |
| I G L D S L L I S F S Y L L I L K T |                 |                 |                 |         |      |
| 819                                 | 828             | 837             | 846             | 855     | 864  |
| GTG TTG GGC TTG ACA                 | CGT GAA GCC CAG | GCC AAG GCA TTT | GGC ACT TGC     | GTC TCT |      |
| V L G L T R E A Q A K A F G T C V S |                 |                 |                 |         |      |
| 873                                 | 882             | 891             | 900             | 909     | 918  |
| CAT GTG TGT GCT GTG                 | TTC ATA TTC TAT | GTA CCT TTC     | ATT GGA TTG     | TCC ATG | GTG  |
| H V C A V F I F Y V P P I G L S M V |                 |                 |                 |         |      |
| 927                                 | 936             | 945             | 954             | 963     | 972  |
| CAT CGC TTT AGC AAG                 | CGG CGT GAC TCT | CCG CTG CCC     | GTC ATC TTG     | GCC AAT | ATC  |
| H R F S K R R D S P L P V I L A N I |                 |                 |                 |         |      |
| 981                                 | 990             | 999             | 1008            | 1017    | 1026 |
| TAT CTG CTG GTT CCT                 | CCT GTG CTC AAC | CCA ATT GTC     | TAT GGA GTG     | AAG ACA | AAG  |
| Y L L V P P V L N P I V Y G V K T K |                 |                 |                 |         |      |
| 1035                                | 1044            | 1053            | 1062            | 1071    | 1080 |
| GAG ATT CGA CAG CGC                 | ATC CTT CGA CTT | TTC CAT GTG     | GCC ACA CAC     | GCT TCA | GAG  |
| E I R Q R I L R L F H V A T H A S E |                 |                 |                 |         |      |
| 1089                                | 1098            | 1107            | 1116            | 1125    | 1134 |
| CCC TAG GTG TCA GTG                 | ATC AAA CTT CTT | TTC CAT TCA     | GAG TCC TCT     | GAT TCA | GAT  |
| P *                                 |                 |                 |                 |         |      |
| 1143                                | 1152            | 1161            | 1170            | 1179    | 1188 |
| TTT AAT GTT AAC ATT                 | TTG GAA GAC AGT | ATT CAG AAA     | AAA AAT TTC     | CTT AAT | AAA  |
| 1197                                | 1206            | 1215            | 1224            | 1233    | 1242 |
| AAA TAC AAC TCA GAT                 | CCT TCA AAT ATG | AAA CTG GTT     | GGG GAA TCT     | CCA TTT | TTT  |
| 1251                                | 1260            | 1269            | 1278            | 1287    | 1296 |
| CAA TAT TAT TTT CTT                 | CTT TGT TTT CTT | GCT ACA TAT     | AAT TAT TAA     | TAC CCT | GAC  |
| 1305                                | 1314            | 1323            | 1332            | 1341    | 1350 |
| TAG GTT GTG GTT GGA                 | GGG TTA TTA CTT | TTC ATT TTA     | CCA TGC AGT     | CCA AAT | CTA  |

FIG. 2C

| 1359        | 1368        | 1377        | 1386        | 1395        | 1404        |
|-------------|-------------|-------------|-------------|-------------|-------------|
| AAC TGC TTC | TAC TGA TGG | TTT ACA GCA | TTC TGA GAT | AAG AAT GGT | ACA TCT AGA |
| 1413        | 1422        | 1431        | 1440        | 1449        | 1458        |
| GAA CAT TTG | CCA AAG GCC | TAA GCA CGG | CAA AGG AAA | ATA AAC ACA | GAA TAT AAT |
| 1467        | 1476        | 1485        | 1494        | 1503        | 1512        |
| AAA ATG AGA | TAA TCT AGC | TTA AAA CTA | TAA CTT CCT | CTT CAG AAC | TCC CAA CCA |
| 1521        | 1530        | 1539        | 1548        | 1557        | 1566        |
| CAT TGG ATC | TCA GAA AAA | TGC TGT CTT | CAA AAT GAC | TTC TAC AGA | GAA GAA ATA |
| 1575        | 1584        | 1593        | 1602        | 1611        | 1620        |
| ATT TTT CCT | CTG GAC ACT | AGC ACT TAA | GGG GAA GAT | TGG AAG TAA | AGC CTT GAA |
| 1629        | 1638        | 1647        | 1656        | 1665        | 1674        |
| AAG AGT ACA | TTT ACC TAC | GTT AAT GAA | AGT TGA CAC | ACT GTT CTG | AGA GTT TTC |
| 1683        | 1692        | 1701        | 1710        | 1719        | 1728        |
| ACA GCA TAT | GGA CCC TGT | TTT TCC TAT | TTA ATT TTC | TTA TCA ACC | CTT TAA TTA |
| 1737        | 1746        | 1755        | 1764        | 1773        | 1782        |
| GGC AAA GAT | ATT ATT AGT | ACC CTC ATT | GTA GCC ATG | GGA AAA TTG | ATG TTC AGT |
| 1791        | 1800        | 1809        | 1818        | 1827        | 1836        |
| GGG GAT CAG | TGA ATT AAA | TGG GGT CAT | ACA AGT ATA | AAA ATT AAA | AAA AAA AAA |
| 1845        | 1854        | 1863        | 1872        | 1881        | 1890        |
| GAC TTC ATG | CCC AAT CTC | ATA TGA TGT | GGA AGA ACT | GTT AGA GAG | ACC AAC AGG |
| 1899        | 1908        | 1917        | 1926        | 1935        | 1944        |
| GTA GTG GGT | TAG AGA TTT | CCA GAG TCT | TAC ATT TTC | TAG AGG AGG | TAT TTA ATT |
| 1953        | 1962        | 1971        | 1980        | 1989        | 1998        |
| TCT TCT CAC | TCA TCC AGT | GTT GTA TTT | AGG AAT TTC | CTG GCA ACA | GAA CTC ATG |
| 2007        | 2016        | 2025        | 2034        | 2043        | 2052        |
| GCT TTA ATC | CCA CTA GCT | ATT GCT TAT | TGT CCT GGT | CCA ATT GCC | AAT TAC CTG |
| 2061        | 2070        | 2079        | 2088        | 2097        | 2106        |
| TGT CTT GGA | AGA AGT GAT | TTC TAG GTT | CAC CAT TAT | GGA AGA TTC | TTA TTC AGA |
| 2115        | 2124        | 2133        | 2142        | 2151        | 2160        |
| AAG TCT GCA | TAG GGC TTA | TAG CAA GTT | ATT TAT TTT | TAA AAG TTC | CAT AGG TGA |
| 2169        | 2178        | 2187        | 2196        | 2205        | 2214        |
| TTC TGA TAG | GCA GTG AGG | TTA GGG AGC | CAC CAG TTA | TGA TGG GAA | GTA TGG AAT |
| 2223        | 2232        | 2241        | 2250        | 2259        | 2268        |
| GGC AGG TCT | TGA AGA TAA | CAT TGG CCT | TTT GAG TGT | GAC TCG TAG | CTG GAA AGT |
| 2277        | 2286        | 2295        | 2304        | 2313        | 2322        |
| GAG GGA ATC | TTC AGG ACC | ATG CTT TAT | TTG GGG CTT | TGT GCA GTA | TGG AAC AGG |
| 2331        | 2340        | 2349        | 2358        | 2367        | 2376        |
| GAC TTT GAG | ACC AGG AAA | GCA ATC TGA | CTT AGG CAT | GGG AAT CAG | GCA TTT TTG |

FIG. 2D

|                         |                             |                         |      |      |      |
|-------------------------|-----------------------------|-------------------------|------|------|------|
| 2385                    | 2394                        | 2403                    | 2412 | 2421 | 2430 |
| CTT CTG AGG GGC TAT TAC | CAA GGG TTA ATA GGT TTC ATC | TTC AAC AGG ATA TGA     |      |      |      |
| 2439                    | 2448                        | 2457                    | 2466 | 2475 | 2484 |
| CAA CAG TGT TAA CCA AGA | AAC TCA AAT TAC AAA TAC     | TAA AAC ATG TGA TCA TAT |      |      |      |
| 2493                    | 2502                        | 2511                    | 2520 | 2529 | 2538 |
| ATG TGG TAA GTT TCA TTT | TCT TTT TCA ATC CTC AGG     | TTC CCT GAT ATG GAT TCC |      |      |      |
| 2547                    | 2556                        | 2565                    | 2574 | 2583 | 2592 |
| TAT AAC ATG CTT TCA TCC | CCT TTT GTA ATG GAT ATC     | ATA TTT GGA AAT GCC TAT |      |      |      |
| 2601                    | 2610                        | 2619                    | 2628 | 2637 | 2646 |
| TTA ATA CTT GTA TTT GCT | GCT GGA CTG TAA GCC CAT     | GAG GGC ACT GTT TAT TAT |      |      |      |
| 2655                    | 2664                        | 2673                    | 2682 | 2691 | 2700 |
| TGA ATG TCA TCT CTG TTC | ATC ATT GAC TGC TCT TTG     | CTC ATC ATT GAA TCC CCC |      |      |      |
| 2709                    | 2718                        | 2727                    | 2736 | 2745 | 2754 |
| AGC AAA GTG CCT AGA ACA | TAA TAG TGC TTA TGC TTG     | ACA CCG GTT ATT TTT CAT |      |      |      |
| 2763                    | 2772                        | 2781                    | 2790 | 2799 | 2808 |
| CAA ACC TGA TTC CTT CTG | TCC TGA ACA CAT AGC CAG     | GCA ATT TTC CAG CCT TCT |      |      |      |
| 2817                    | 2826                        | 2835                    | 2844 | 2853 | 2862 |
| TTG AGT TGG GTA TTA TTA | AAT TCT GGC CAT TAC TTC     | CAA TGT GAG TGG AAG TGA |      |      |      |
| 2871                    | 2880                        | 2889                    | 2898 | 2907 | 2916 |
| CAT GTG CAA TTT CTA TAC | CTG GCT CAT AAA ACC CTC     | CCA TGT GCA GCC TTT CAT |      |      |      |
| 2925                    | 2934                        | 2943                    | 2952 | 2961 | 2970 |
| GTT GAC ATT AAA TGT GAC | TTG GGA AGC TAT GTG TTA     | CAC AGA GTA AAT CAC CAG |      |      |      |
| 2979                    | 2988                        | 2997                    | 3006 | 3015 | 3024 |
| AAG CCT GGA TTT CTG AAA | AAA CTG TGC AGA GCC AAA     | CCT CTG TCA TTT GCA ACT |      |      |      |
| 3033                    | 3042                        | 3051                    | 3060 | 3069 | 3078 |
| CCC ACT TGT ATT TGT ACG | AGG CAG TTG GAT AAG TGA     | AAA ATA AAG TAC TAT TGT |      |      |      |
| 3087                    | 3096                        | 3105                    | 3114 | 3123 | 3132 |
| GTC AAG AAA AAA AAA AAA | AAA AAA AAA AAA AAA AAA     | AAA AAA AAA AAA AAA AAA |      |      |      |

AAA A 3'

Figure 3: Protein Sequence for 101P3A11 (*piece of SEQ ID NO: 2880*)

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI  
STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRTKIGV  
AAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDVMKLACDDIRVNVVYGLIVISAIGLDSLLISFSYL  
LILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHFRFSKRDSPLPVILANIYLLVPPVLNPIVYG  
VKTKEIRQRILRLFHVATHASEP

Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

Query: 34 GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIVLIRTSPQLHTPMYLF 93  
 GN + T FIL+GL L +Y + ++GNL II ++RT LH PMY+FL  
 Sbjct: 6 GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL 65

Query: 94 SHLAFLDIGYSSSVTPIMLRGFLRKGT FIPVAGCVAQLCIVVAFGTSESFLLASMAYDRY 153  
 L+ +DI S+S P ML F T I C+ Q+ + + ES +L +MA+DRY  
 Sbjct: 66 CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125

Query: 154 VAICSPLLYSTQMSSTVCILLVGTSYLGWVNAWIFTGCSLNL SFCGPNKINHFFCDYSP 213  
 VAIC PL ++T ++ + + + G L FC N ++H +C +  
 Sbjct: 126 VAICHPLRHATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD 185

Query: 214 LLKLSCSHDFSFEVIPAISSGSIIVTVFIIALSYVYILVSILKMRSTEGRQKAFSTCTS 273  
 ++KL+C V I S I + +I+ SY+ IL ++L + + E + KAF TC S  
 Sbjct: 186 VMKLACDDIRVNVVYGLIIVISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244

Query: 274 HLTAVTLFFGTITFIYVMPQSSYSTDQNK----VVSVFYTVVIPMLNPLIYSFRNKEVKE 329  
 H+ AV +F+ + FI + +S ++ +++ Y +V P+LNP++Y + KE+++  
 Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQ 302

Query: 330 AMKKL 334 (SEQ ID NO: 2881)  
 + +L  
 Sbjct: 303 RILRL 307 (SEQ ID NO: 2882)

Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73  
 F+LIG+PGLEEA FW FPL S+Y +A+ GN +++IVRTE SLH PMY+FLCML+ ID+  
 RA1C: 11 FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133  
 +STS+MPK+LA+FWF+S I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR  
 RA1C: 71 ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPRTVKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCIHQDVMKLACDD 193  
 HA VL +IG+ A+VRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D  
 RA1C: 131 HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190

PHOR: 194 IRVNVVYGLIIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252  
 NVVYGL I+ +G+D + IS SY LI++ VL L ++ +AKAFGTCVSH+ V F  
 RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLA F 250

PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKAIRQRILRLFHVA 311 (SEQ ID NO: 2223)  
 YVP IGLS+VHRF D + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++  
 RA1C: 251 YVPLIGLSVVHRFGNSLDPIVHVLMGDVYLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO: 2274)



Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR. (gi|13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73  
 F+LIG+PGLE+A FW+ FPL S+Y++A+ GN +++IVRTE SLH PMY+FLCML+ ID+

GPCR: 11 FVLIGIPGLEKAHFWVGFPLLSMYVVMFGNCIVVFIVRTERS LHAPMYLFLCMLAIDL 70

PHOR: 74 LISTSSMPKMLAIFWFNSTTIOFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133  
 +STS+MPK+LA+FWF+S I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR

GPCR: 71 ALSTSTMPKILALFWFDSREISFEACLTQMFFIHLSAESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCSRNLSSHYSYCLHQDVMKLACDD 193  
 HA VL +IG+ AVVRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D

GPCR: 131 HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190

PHOR: 194 IRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252  
 NVVYGL I+ +G+D + IS SY LI++TVL L ++ +AKAFGTCVSH+ V F

GPCR: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLA 250

PHOR: 253 YVPFIGLSMVHRFSKRDSPLPVILANIYLLVPPVLNPIVYGVTKEIRQRILRLFHVA 311 (SEQ ID NO: 2885)  
 YVP IGLS+VHRF + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++

GPCR: 251 YVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLPPVINPIYGAKTKQIRTVLAMFKIS 309 (SEQ ID NO: 2886)

Figure 25: Alignment with human olfactory receptor 5II12 (gi|14423836)

Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

PHOR: 7 NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66  
 N + +F+L G+PGLE + WL+ PLC +Y +A+ GN I+ VR E SLHEPMY FL  
 HOR5: 5 NVTHPAFFLLTGIPGLESSHWSLGLCVMYAVALGGNTVILQAVRVEPSLHEPMYFSL 64

PHOR: 67 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126  
 MLS D+ IS +++P +L F N+ I FDACL+Q+F IH S MES +LLAM+FDYV  
 HOR5: 65 MLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMESGILLAMSFDRYV 124

PHOR: 127 AICHPLRHATVLTTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186  
 AIC PLR+ATVLT + +G+ A R + PLP IK+LP CRSN+LSHSYCLH D+  
 HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLPLPFLIKRLPICRSNVLSHSYCLHPDM 184

PHOR: 187 MKLACDDIRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245  
 M+LAC DI +N +YGL V++S G+D I SY+LIL++V+ +RE + KA TCVSH  
 HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244

PHOR: 246 VCAVFIFYVPFGLSMVHRFSKRDSPLPVILANIYLLVPPVLNPIVYGVTKEIRQRIL 305  
 + AV FYVP IG+S VHRF K + V+++N+YL VPPVLNP++Y KTKEIR+ I  
 HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHVLSNVYLFVPPVLNPLIYSAKTKEIRRAIF 304

PHOR: 306 RLFH 309 (SEQ ID NO: 2887)  
 R+FH  
 HOR5: 305 RMFH 308 (SEQ ID NO: 2888)